

SI TABLE S4

**Relative expression ratios of significantly-changed proteins in PC3-LN4 cells by 72hr drug treatments**  
 (142 altered proteins that were common for all treated groups are highlighted with shadow)

Accession Number	Protein Name	KX01 treatment			KX02 treatment			Vinblastine treatment			Go Annotation (Biological Process)
		Ratio	StdDev	p Value	Ratio	StdDev	p Value	Ratio	StdDev	p Value	
P06703	Protein S100-A6	1.57	0.32	< 0.01	1.58	0.30	< 0.01	1.74	0.31	< 0.01	Cell cycle
O95347	Structural maintenance of chromosomes protein 2	0.71	0.15	0.05	0.61	0.11	< 0.01	0.58	0.13	< 0.01	Cell cycle
P16949	Stathmin	0.66	0.05	< 0.01	0.60	0.07	< 0.01	0.68	0.06	< 0.01	Cell cycle
Q9NTJ3	Structural maintenance of chromosomes protein 4	0.59	0.21	< 0.01	0.59	0.25	0.02	0.52	0.14	< 0.01	Cell cycle
Q13885	Tubulin beta-2A chain	0.51	0.02	< 0.01	0.56	0.02	< 0.01	0.58	0.02	< 0.01	Cell cycle
O00743	Serine/threonine-protein phosphatase 6	0.61	0.17	< 0.01	0.55	0.12	< 0.01	0.63	0.13	< 0.01	Cell cycle; Protein metabolic process
Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase	0.51	0.08	< 0.01	0.40	0.06	< 0.01	0.40	0.06	< 0.01	Cell cycle; Protein metabolic process
P06493	Cell division control protein 2 homolog	0.50	0.06	< 0.01	0.47	0.06	< 0.01	0.41	0.04	< 0.01	Cell cycle; Protein metabolic process; Response to stimulus
P62979	40S ribosomal protein S27a	0.56	0.29	< 0.01	0.56	0.41	< 0.01	0.59	0.41	< 0.01	Cell cycle; Protein metabolic process; Translation
P24941	Cell division protein kinase 2	0.52	0.13	< 0.01	0.47	0.10	< 0.01	0.48	0.11	< 0.01	Cell cycle; Protein metabolic process; Transport
Q13509	Tubulin beta-3 chain	0.54	0.02	< 0.01	0.58	0.03	< 0.01	0.60	0.02	< 0.01	Cell cycle; Response to stimulus
P07437	Tubulin beta chain	0.50	0.02	< 0.01	0.54	0.02	< 0.01	0.56	0.02	< 0.01	Cell cycle; Response to stimulus
P51610	Host cell factor	0.59	0.21	< 0.01	0.59	0.21	< 0.01	0.69	0.19	< 0.01	Cell cycle; RNA metabolic process; Transcription
Q8IX12	Cell division cycle and apoptosis regulator protein 1	0.59	0.21	< 0.01	0.60	0.26	0.02	0.70	0.16	0.02	Cell cycle; RNA metabolic process; Transcription
P52926	High mobility group protein HMGI-C	1.70	2.14	< 0.01	1.69	1.63	< 0.01	2.10	1.84	< 0.01	Cell cycle; Transcription
Q14566	DNA replication licensing factor MCM6	0.66	0.09	< 0.01	0.59	0.09	< 0.01	0.53	0.07	< 0.01	Cell cycle; Transcription
P25205	DNA replication licensing factor MCM3	0.63	0.08	< 0.01	0.52	0.08	< 0.01	0.55	0.07	< 0.01	Cell cycle; Transcription
P05783	Keratin, type I cytoskeletal 18	0.50	0.03	< 0.01	0.48	0.03	< 0.01	0.61	0.03	< 0.01	Cell cycle; Transport
P61009	Signal peptidase complex subunit 3	0.70	0.17	< 0.01	0.62	0.15	< 0.01	0.58	0.13	< 0.01	Protein metabolic process
P52888	Thimet oligopeptidase	0.68	0.16	< 0.01	0.64	0.19	< 0.01	0.69	0.15	< 0.01	Protein metabolic process
P27708	CAD protein	0.65	0.06	< 0.01	0.63	0.07	< 0.01	0.53	0.05	< 0.01	Protein metabolic process
Q9C0C9	Ubiquitin-conjugating enzyme E2 O	0.65	0.08	< 0.01	0.62	0.09	< 0.01	0.64	0.07	< 0.01	Protein metabolic process
Q04323	UBX domain-containing protein 1	0.59	0.15	< 0.01	0.59	0.14	< 0.01	0.61	0.13	< 0.01	Protein metabolic process
Q9NZL4	Hsp70-binding protein 1	0.58	0.17	0.02	0.58	0.20	0.02	0.66	0.17	< 0.01	Protein metabolic process

O14929	Histone acetyltransferase type B catalytic subunit	0.56	0.09	< 0.01	0.51	0.13	< 0.01	0.50	0.08	< 0.01	Protein metabolic process
P22681	E3 ubiquitin-protein ligase CBL	0.46	0.25	< 0.01	0.29	0.18	< 0.01	0.53	0.25	< 0.01	Protein metabolic process
O95757	Heat shock 70 kDa protein 4L	0.66	0.05	< 0.01	0.61	0.05	< 0.01	0.62	0.04	< 0.01	Protein metabolic process; Response to stimulus
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	0.54	0.30	< 0.01	0.48	0.19	< 0.01	0.48	0.25	< 0.01	Protein metabolic process; Response to stimulus
P62244	40S ribosomal protein S15a	0.68	0.08	< 0.01	0.60	0.07	< 0.01	0.68	0.07	< 0.01	Protein metabolic process; Response to stimulus; Translation
P98179	Putative RNA-binding protein 3	0.31	0.07	< 0.01	0.32	0.08	< 0.01	0.64	0.12	< 0.01	Protein metabolic process; RNA metabolic process; Response to stimulus; Translation
P62263	40S ribosomal protein S14	0.70	0.07	< 0.01	0.58	0.08	< 0.01	0.71	0.06	< 0.01	Protein metabolic process; RNA metabolic process; Translation
Q04637	Eukaryotic translation initiation factor 4 gamma 1	0.69	0.07	< 0.01	0.70	0.08	< 0.01	0.62	0.05	< 0.01	Protein metabolic process; RNA metabolic process; Translation
P62906	60S ribosomal protein L10a	0.66	0.07	< 0.01	0.60	0.08	< 0.01	0.68	0.07	< 0.01	Protein metabolic process; RNA metabolic process; Translation
P18124	60S ribosomal protein L7	0.62	0.08	< 0.01	0.58	0.08	< 0.01	0.70	0.08	< 0.01	Protein metabolic process; RNA metabolic process; Translation
P61254	60S ribosomal protein L26	0.61	0.08	< 0.01	0.54	0.08	< 0.01	0.68	0.08	< 0.01	Protein metabolic process; RNA metabolic process; Translation
P18077	60S ribosomal protein L35a	0.57	0.15	< 0.01	0.50	0.11	< 0.01	0.62	0.14	< 0.01	Protein metabolic process; RNA metabolic process; Translation
P62913	60S ribosomal protein L11	0.62	0.08	< 0.01	0.55	0.08	< 0.01	0.70	0.07	< 0.01	Protein metabolic process; RNA metabolic process; Transport; Translation
P15880	40S ribosomal protein S2	0.70	0.10	< 0.01	0.62	0.08	< 0.01	0.68	0.08	< 0.01	Protein metabolic process; Translation
P62277	40S ribosomal protein S13	0.69	0.09	< 0.01	0.58	0.07	< 0.01	0.71	0.07	< 0.01	Protein metabolic process; Translation

Q96RP9	Elongation factor G 1, mitochondrial	0.67	0.14	< 0.01	0.60	0.11	< 0.01	0.71	0.14	< 0.01	Protein metabolic process; Translation
Q02878	60S ribosomal protein L6	0.63	0.05	< 0.01	0.66	0.06	< 0.01	0.71	0.05	< 0.01	Protein metabolic process; Translation
P61313	60S ribosomal protein L15	0.62	0.11	< 0.01	0.55	0.10	< 0.01	0.67	0.09	< 0.01	Protein metabolic process; Translation
P60866	40S ribosomal protein S20	0.62	0.18	0.01	0.54	0.16	< 0.01	0.65	0.16	< 0.01	Protein metabolic process; Translation
P27635	60S ribosomal protein L10	0.62	0.10	< 0.01	0.55	0.09	< 0.01	0.71	0.11	< 0.01	Protein metabolic process; Translation
P36578	60S ribosomal protein L4	0.61	0.05	< 0.01	0.61	0.06	< 0.01	0.70	0.06	< 0.01	Protein metabolic process; Translation
P62899	60S ribosomal protein L31	0.60	0.10	< 0.01	0.55	0.08	< 0.01	0.62	0.09	< 0.01	Protein metabolic process; Translation
P18621	60S ribosomal protein L17	0.60	0.06	< 0.01	0.52	0.07	< 0.01	0.66	0.08	< 0.01	Protein metabolic process; Translation
P42766	60S ribosomal protein L35	0.57	0.15	< 0.01	0.59	0.13	< 0.01	0.63	0.13	< 0.01	Protein metabolic process; Translation
P46779	60S ribosomal protein L28	0.54	0.11	< 0.01	0.49	0.09	< 0.01	0.66	0.13	< 0.01	Protein metabolic process; Translation
P61513	60S ribosomal protein L37a	0.53	0.14	< 0.01	0.45	0.12	< 0.01	0.71	0.20	< 0.01	Protein metabolic process; Translation
Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50	0.69	0.19	< 0.01	0.64	0.17	< 0.01	0.61	0.14	< 0.01	Protein metabolic process; Transport
P49792	E3 SUMO-protein ligase RanBP2	0.58	0.12	< 0.01	0.61	0.10	< 0.01	0.60	0.10	< 0.01	Protein metabolic process; Transport
P25815	Protein S100-P	1.85	0.40	< 0.01	1.81	0.31	< 0.01	3.24	0.51	< 0.01	Response to stimulus
P61769	Beta-2-microglobulin	1.73	0.63	< 0.01	1.44	0.48	< 0.01	1.65	0.51	< 0.01	Response to stimulus
P46821	Microtubule-associated protein 1B	0.67	0.08	< 0.01	0.68	0.09	< 0.01	0.67	0.08	< 0.01	Response to stimulus
Q9UDY2	Tight junction protein ZO-2	0.66	0.18	0.03	0.54	0.13	< 0.01	0.67	0.15	< 0.01	Response to stimulus
Q12929	Epidermal growth factor receptor kinase substrate 8	0.63	0.18	0.01	0.53	0.24	< 0.01	0.61	0.16	< 0.01	Response to stimulus
P48681	Nestin	0.61	0.03	< 0.01	0.55	0.03	< 0.01	0.68	0.03	< 0.01	Response to stimulus
P68371	Tubulin beta-2C chain	0.52	0.02	< 0.01	0.57	0.02	< 0.01	0.59	0.02	< 0.01	Response to stimulus
P16989	DNA-binding protein A	0.54	0.05	< 0.01	0.58	0.06	< 0.01	0.66	0.06	< 0.01	Response to stimulus; Transcription
P37198	Nuclear pore glycoprotein p62	0.69	0.21	< 0.01	0.66	0.22	< 0.01	0.69	0.17	< 0.01	Response to stimulus; Transport
O00442	RNA 3'-terminal phosphate cyclase	1.97	2.21	< 0.01	1.47	1.72	0.01	1.91	2.01	< 0.01	RNA metabolic process
Q9BXR0	Queuine tRNA-ribosyltransferase	0.68	0.13	0.03	0.67	0.15	0.03	0.69	0.11	< 0.01	RNA metabolic process
Q9H0S4	Probable ATP-dependent RNA helicase DDX47	0.63	0.13	< 0.01	0.62	0.17	< 0.01	0.69	0.17	< 0.01	RNA metabolic process

Q13242	Splicing factor, arginine/serine-rich 9	0.62	0.11	< 0.01	0.60	0.14	< 0.01	0.71	0.13	< 0.01	RNA metabolic process
Q8N8A6	ATP-dependent RNA helicase DDX51	0.59	0.15	< 0.01	0.62	0.11	< 0.01	0.58	0.11	< 0.01	RNA metabolic process
Q12849	G-rich sequence factor 1	0.59	0.08	< 0.01	0.54	0.09	< 0.01	0.51	0.07	< 0.01	RNA metabolic process
Q99575	Ribonucleases P/MRP protein subunit POP1	0.57	0.13	< 0.01	0.58	0.17	< 0.01	0.59	0.11	< 0.01	RNA metabolic process
O00567	Nucleolar protein 5A	0.54	0.05	< 0.01	0.59	0.06	< 0.01	0.66	0.06	< 0.01	RNA metabolic process
Q9NW13	RNA-binding protein 28	0.43	0.15	< 0.01	0.45	0.15	< 0.01	0.69	0.20	< 0.01	RNA metabolic process
Q9BVJ6	U3 small nucleolar RNA-associated protein 14 homolog A	0.33	0.05	< 0.01	0.32	0.06	< 0.01	0.61	0.07	< 0.01	RNA metabolic process
Q14690	Protein RRP5 homolog	0.27	0.18	< 0.01	0.42	0.27	< 0.01	0.51	0.24	0.01	RNA metabolic process
P39748	Flap endonuclease 1	0.63	0.06	< 0.01	0.56	0.07	< 0.01	0.70	0.06	< 0.01	RNA metabolic process; Response to stimulus
Q13951	Core-binding factor subunit beta	0.68	0.17	0.04	0.63	0.26	0.03	0.70	0.20	0.02	RNA metabolic process; Transcription
P78347	General transcription factor II-I	0.50	0.15	< 0.01	0.54	0.12	< 0.01	0.62	0.13	< 0.01	RNA metabolic process; Transcription
P67809	Nuclease-sensitive element-binding protein 1	0.46	0.03	< 0.01	0.53	0.04	< 0.01	0.64	0.04	< 0.01	RNA metabolic process; Transcription
O75494	FUS-interacting serine-arginine-rich protein 1	0.70	0.13	< 0.01	0.59	0.14	< 0.01	0.62	0.11	< 0.01	RNA metabolic process; Transport
Q14839	Chromodomain-helicase-DNA-binding protein 4	0.68	0.14	< 0.01	0.62	0.11	< 0.01	0.62	0.11	< 0.01	Transcription
P33991	DNA replication licensing factor MCM4	0.67	0.10	< 0.01	0.65	0.14	< 0.01	0.56	0.10	< 0.01	Transcription
P06454	Prothymosin alpha	0.66	0.09	< 0.01	0.50	0.10	< 0.01	0.61	0.08	< 0.01	Transcription
Q8WXI9	Transcriptional repressor p66-beta	0.66	0.08	< 0.01	0.62	0.11	< 0.01	0.61	0.11	< 0.01	Transcription
P42704	Leucine-rich PPR motif-containing protein, mitochondrial	0.63	0.03	< 0.01	0.61	0.03	< 0.01	0.71	0.02	< 0.01	Transcription; Transport
O95994	Anterior gradient protein 2 homolog	1.45	0.26	< 0.01	1.52	0.28	< 0.01	2.73	0.45	< 0.01	Transport
Q8TEX9	Importin-4	0.67	0.08	< 0.01	0.63	0.08	< 0.01	0.65	0.06	< 0.01	Transport
Q9NP72	Ras-related protein Rab-18	0.65	0.10	< 0.01	0.65	0.12	< 0.01	0.66	0.09	< 0.01	Transport
P35658	Nuclear pore complex protein Nup214	0.64	0.16	< 0.01	0.67	0.20	< 0.01	0.70	0.18	< 0.01	Transport
P29373	Cellular retinoic acid-binding protein 2	0.62	0.08	< 0.01	0.58	0.07	< 0.01	0.59	0.07	< 0.01	Transport
Q13283	Ras GTPase-activating protein-binding protein 1	0.59	0.08	< 0.01	0.59	0.10	< 0.01	0.71	0.09	< 0.01	Transport
P33897	ATP-binding cassette sub-family D member 1	0.55	0.11	< 0.01	0.63	0.13	< 0.01	0.64	0.11	< 0.01	Transport
Q99567	Nuclear pore complex protein Nup88	0.55	0.30	< 0.01	0.62	0.32	< 0.01	0.60	0.24	< 0.01	Transport
Q00341	Vigilin	0.54	0.10	< 0.01	0.60	0.09	< 0.01	0.63	0.08	< 0.01	Transport
Q01650	Large neutral amino acids transporter small subunit 1	0.53	0.13	< 0.01	0.50	0.11	< 0.01	0.68	0.15	< 0.01	Transport
Q15758	Neutral amino acid transporter B(0)	0.50	0.07	< 0.01	0.52	0.09	< 0.01	0.63	0.07	< 0.01	Transport
Q8IVF2	Protein AHNAK2	2.26	1.33	< 0.01	2.99	1.94	< 0.01	3.90	1.62	< 0.01	multicellular organismal development
P60903	Protein S100-A10	1.89	0.27	< 0.01	1.97	0.34	< 0.01	1.74	0.29	< 0.01	signal transduction

P31949	Protein S100-A11	1.56	0.24	< 0.01	1.57	0.25	< 0.01	1.84	0.24	< 0.01	regulation of DNA replication
Q9UBB4	Ataxin-10	0.71	0.16	< 0.01	0.68	0.14	< 0.01	0.67	0.13	< 0.01	multicellular organismal development
P22234	Multifunctional protein ADE2	0.70	0.05	< 0.01	0.66	0.06	< 0.01	0.66	0.05	< 0.01	nucleobase
P12268	Inosine-5'-monophosphate dehydrogenase 2	0.68	0.09	< 0.01	0.63	0.08	< 0.01	0.61	0.07	< 0.01	cell activation
O60610	Protein diaphanous homolog 1	0.67	0.16	0.03	0.66	0.15	0.04	0.65	0.15	< 0.01	system process
Q14444	Caprin-1	0.65	0.08	< 0.01	0.71	0.09	< 0.01	0.69	0.07	< 0.01	unknown
Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	0.65	0.07	< 0.01	0.63	0.08	< 0.01	0.66	0.07	< 0.01	multicellular organismal development
Q8IY67	Ribonucleoprotein PTB-binding 1	0.65	0.14	0.01	0.64	0.15	< 0.01	0.70	0.12	< 0.01	unknown
P19623	Spermidine synthase	0.64	0.10	< 0.01	0.52	0.10	< 0.01	0.65	0.11	< 0.01	cellular amino acid and derivative metabolic process
P11908	Ribose-phosphate pyrophosphokinase 2	0.64	0.06	< 0.01	0.61	0.06	< 0.01	0.61	0.04	< 0.01	nucleobase
Q6NXE6	Armadillo repeat-containing protein 6	0.64	0.13	< 0.01	0.54	0.08	< 0.01	0.70	0.10	< 0.01	unknown
Q9H773	XTP3-transactivated gene A protein	0.64	0.14	< 0.01	0.61	0.14	< 0.01	0.64	0.16	< 0.01	protein complex assembly
Q16850	Cytochrome P450 51A1	0.64	0.11	< 0.01	0.59	0.11	< 0.01	0.58	0.07	< 0.01	alcohol metabolic process
P16724		0.63	0.30	< 0.01	0.55	0.18	< 0.01	0.56	0.18	< 0.01	unknown
Q14195	Dihydropyrimidinase-related protein 3	0.63	0.14	0.02	0.64	0.14	< 0.01	0.62	0.15	< 0.01	nucleobase
P23921	Ribonucleoside-diphosphate reductase large subunit	0.61	0.08	< 0.01	0.59	0.08	< 0.01	0.45	0.07	< 0.01	nucleobase
Q9H910	Hematological and neurological expressed 1-like protein	0.60	0.16	< 0.01	0.58	0.17	< 0.01	0.71	0.13	< 0.01	unknown
Q8WWM7	Ataxin-2-like protein	0.59	0.10	< 0.01	0.64	0.11	< 0.01	0.71	0.12	< 0.01	unknown
O95425	Supervillin	0.59	0.10	< 0.01	0.66	0.17	< 0.01	0.61	0.08	< 0.01	organelle organization
Q9UFH2	Dynein heavy chain 17, axonemal	0.59	0.08	< 0.01	0.59	0.10	< 0.01	0.60	0.07	< 0.01	ciliary or flagellar motility
Q27J81	Inverted formin-2	0.59	0.09	< 0.01	0.65	0.10	< 0.01	0.67	0.09	< 0.01	organelle organization
O94776	Metastasis-associated protein MTA2	0.59	0.12	< 0.01	0.47	0.08	< 0.01	0.63	0.06	< 0.01	negative regulation of transcription from RNA polymerase II promoter
Q9BQE3	Tubulin alpha-1C chain	0.56	0.02	< 0.01	0.56	0.02	< 0.01	0.57	0.02	< 0.01	protein complex assembly
P42166	Lamina-associated polypeptide 2 isoform alpha	0.56	0.04	< 0.01	0.45	0.04	< 0.01	0.62	0.03	< 0.01	regulation of biosynthetic process
P68363	Tubulin alpha-1B chain	0.56	0.02	< 0.01	0.55	0.02	< 0.01	0.57	0.01	< 0.01	microtubule cytoskeleton organization
P35520	Cystathionine beta-synthase	0.55	0.21	< 0.01	0.54	0.25	< 0.01	0.67	0.22	0.03	sulfur amino acid metabolic process
P45973	Chromobox protein homolog 5	0.55	0.14	< 0.01	0.64	0.13	< 0.01	0.66	0.12	< 0.01	chromatin organization

Q15942	Zyxin	0.55	0.06	< 0.01	0.56	0.05	< 0.01	0.60	0.05	< 0.01	cell communication
Q71RC2	La-related protein 4	0.54	0.10	< 0.01	0.57	0.11	< 0.01	0.66	0.11	< 0.01	unknown
P30085	UMP-CMP kinase	0.53	0.12	< 0.01	0.38	0.08	< 0.01	0.70	0.13	< 0.01	nucleobase
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma	0.53	0.05	< 0.01	0.43	0.05	< 0.01	0.65	0.04	< 0.01	regulation of biosynthetic process
Q9BUF5	Tubulin beta-6 chain	0.53	0.04	< 0.01	0.56	0.05	< 0.01	0.61	0.04	< 0.01	protein complex assembly
Q96KN1	Protein FAM84B	0.51	0.11	< 0.01	0.52	0.12	< 0.01	0.63	0.10	< 0.01	unknown
P68366	Tubulin alpha-4A chain	0.51	0.02	< 0.01	0.53	0.02	< 0.01	0.51	0.02	< 0.01	protein complex assembly
Q9Y3Y2	Uncharacterized protein C1orf77	0.51	0.12	< 0.01	0.54	0.13	< 0.01	0.63	0.14	0.02	unknown
Q6PKG0	La-related protein 1	0.50	0.26	< 0.01	0.52	0.33	0.02	0.64	0.25	0.02	unknown
Q9UK76	Hematological and neurological expressed 1 protein	0.50	0.22	< 0.01	0.50	0.23	0.01	0.46	0.19	< 0.01	unknown
Q06203	Amidophosphoribosyltransferase	0.47	0.10	< 0.01	0.49	0.14	< 0.01	0.59	0.14	< 0.01	organic acid metabolic process
P10412	Histone H1.4	0.43	0.06	< 0.01	0.36	0.05	< 0.01	0.48	0.06	< 0.01	DNA packaging
Q9Y617	Phosphoserine aminotransferase	0.42	0.06	< 0.01	0.40	0.06	< 0.01	0.60	0.08	< 0.01	organic acid metabolic process
Q99848	Probable rRNA-processing protein EBP2	0.41	0.07	< 0.01	0.42	0.08	< 0.01	0.65	0.10	< 0.01	cellular process
P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	0.40	0.06	< 0.01	0.31	0.06	< 0.01	0.36	0.06	< 0.01	nucleobase
O15213	WD repeat-containing protein 46	0.35	0.11	< 0.01	0.42	0.12	< 0.01	0.55	0.13	< 0.01	unknown
Q6ZU35	Uncharacterized protein KIAA1211	0.33	0.06	< 0.01	0.24	0.04	< 0.01	0.36	0.06	< 0.01	unknown
Q8TD30	Alanine aminotransferase 2	0.28	0.07	< 0.01	0.28	0.06	< 0.01	0.55	0.11	< 0.01	metabolic process
Q8WTT2	Nucleolar complex protein 3 homolog	0.28	0.11	< 0.01	0.39	0.12	< 0.01	0.57	0.11	< 0.01	cellular process
Q1L6U9	PC3-secreted microprotein	0.11	0.04	< 0.01	0.19	0.06	< 0.01	0.54	0.12	< 0.01	unknown
Q14764	Major vault protein	1.24	0.31	< 0.01	1.60	0.43	< 0.01	1.58	0.34	< 0.01	
P17301	Integrin alpha-2	1.14	0.61	< 0.01	1.45	0.79	< 0.01	1.58	0.61	< 0.01	
P08174	Complement decay-accelerating factor	1.27	0.53	< 0.01	1.41	0.62	< 0.01	2.80	1.84	< 0.01	
Q9BPW8	Protein NipSnap homolog 1	1.44	0.26	< 0.01	1.35	0.32	< 0.01	1.61	0.27	< 0.01	
P07602	Proactivator polypeptide	1.32	0.70	< 0.01	1.33	0.79	< 0.01	1.74	0.76	< 0.01	
Q96BM9	ADP-ribosylation factor-like protein 8A	1.23	0.97	< 0.01	1.32	1.00	0.01	1.73	1.24	< 0.01	
P32320	Cytidine deaminase	1.58	0.24	< 0.01	1.32	0.18	< 0.01	1.47	0.20	< 0.01	
P32189	Glycerol kinase	1.43	0.39	< 0.01	1.31	0.35	< 0.01	1.71	0.44	< 0.01	
Q14108	Lysosome membrane protein 2	1.17	0.26	< 0.01	1.29	0.29	< 0.01	1.53	0.29	< 0.01	
P45880	Voltage-dependent anion-selective channel protein 2	1.32	0.05	< 0.01	1.29	0.05	< 0.01	1.42	0.05	< 0.01	
Q9Y3D6	Mitochondrial fission 1 protein	1.32	0.20	< 0.01	1.29	0.26	< 0.01	1.53	0.20	< 0.01	
P07858	Cathepsin B	1.21	0.25	< 0.01	1.27	0.32	< 0.01	1.58	0.30	< 0.01	
P13987	CD59 glycoprotein	1.14	0.21	< 0.01	1.26	0.25	< 0.01	1.66	0.36	< 0.01	
Q92597	Protein NDRG1	1.28	0.14	< 0.01	1.24	0.17	< 0.01	1.64	0.22	< 0.01	
P30740	Leukocyte elastase inhibitor	1.19	0.17	< 0.01	1.23	0.20	< 0.01	1.57	0.21	< 0.01	
Q9NPJ3	Thioesterase superfamily member 2	1.29	0.24	< 0.01	1.22	0.29	< 0.01	1.51	0.28	< 0.01	
Q96A26	UPF0389 protein FAM162A	1.18	0.25	< 0.01	1.21	0.27	< 0.01	1.45	0.26	< 0.01	
P04083	Annexin A1	1.27	0.06	< 0.01	1.20	0.06	< 0.01	1.53	0.06	< 0.01	
P61421	V-type proton ATPase subunit d 1	1.16	0.29	< 0.01	1.16	0.43	< 0.01	1.40	0.33	< 0.01	

O60220	Mitochondrial import inner membrane translocase subunit Tim8 A	1.48	1.01	0.05	1.12	0.44	0.01	1.60	0.81	0.02
P08727	Keratin, type I cytoskeletal 19	1.12	0.07	< 0.01	1.11	0.08	< 0.01	1.43	0.06	< 0.01
Q15847	Adipose most abundant gene transcript 2 protein	1.16	0.18	< 0.01	1.09	0.21	< 0.01	1.72	0.23	< 0.01
Q96FQ6	Protein S100-A16	1.18	0.21	< 0.01	1.09	0.18	< 0.01	1.40	0.19	< 0.01
P17096	High mobility group protein HMG-I/HMG-Y	1.01	0.19	< 0.01	1.07	0.21	< 0.01	1.47	0.22	< 0.01
Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial	1.17	0.46	< 0.01	1.04	0.44	< 0.01	1.53	0.54	< 0.01
P35754	Glutaredoxin-1	1.11	0.21	< 0.01	1.03	0.18	< 0.01	1.45	0.23	< 0.01
Q96BW9	MMP37-like protein, mitochondrial	1.17	0.16	< 0.01	1.01	0.22	< 0.01	1.41	0.14	< 0.01
P68400	Casein kinase II subunit alpha	1.42	0.18	< 0.01	1.24	0.19	< 0.01	1.32	0.17	< 0.01
Q9H9J2	39S ribosomal protein L44, mitochondrial	1.58	0.21	< 0.01	1.31	0.21	< 0.01	1.30	0.21	< 0.01
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	0.54	0.11	< 0.01	0.47	0.09	< 0.01	1.25	0.21	< 0.01
P07108	Acyl-CoA-binding protein	1.52	0.44	< 0.01	1.42	0.50	< 0.01	1.21	0.31	< 0.01
P36957	Dihydrolipoylelysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	1.52	0.30	< 0.01	1.43	0.33	< 0.01	1.19	0.22	< 0.01
P02768	Serum albumin	1.32	0.19	< 0.01	1.68	0.23	< 0.01	1.19	0.18	< 0.01
P13693	Translationally-controlled tumor protein	1.56	0.24	< 0.01	1.38	0.22	< 0.01	1.17	0.18	< 0.01
Q16666	Gamma-interferon-inducible protein Ifi-16	0.54	0.15	< 0.01	0.53	0.18	< 0.01	1.14	0.26	< 0.01
Q16763	Ubiquitin-conjugating enzyme E2 S	2.02	0.53	< 0.01	1.52	0.42	< 0.01	1.11	0.20	< 0.01
Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	1.77	0.56	< 0.01	1.65	0.26	< 0.01	1.10	0.30	0.01
P08754	Guanine nucleotide-binding protein G(k) subunit alpha	0.68	0.14	< 0.01	0.79	0.15	< 0.01	1.05	0.18	< 0.01
O00273	DNA fragmentation factor subunit alpha	0.93	0.21	0.31	0.70	0.22	< 0.01	1.05	0.17	0.04
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.85	0.10	< 0.01	0.69	0.09	< 0.01	1.04	0.11	< 0.01
P04899	Guanine nucleotide-binding protein G(i), alpha-2 subunit	0.69	0.09	< 0.01	0.73	0.10	< 0.01	1.04	0.12	< 0.01
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	0.84	0.08	0.03	0.71	0.07	< 0.01	1.03	0.10	< 0.01
P62995	Splicing factor, arginine/serine-rich 10	0.80	0.10	0.01	0.68	0.07	< 0.01	1.02	0.14	< 0.01
P49591	Seryl-tRNA synthetase, cytoplasmic	0.69	0.09	< 0.01	0.70	0.09	0.01	1.01	0.10	< 0.01
P53597	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial	0.85	0.13	0.90	0.71	0.12	< 0.01	1.01	0.10	< 0.01
P35659	Protein DEK	0.89	0.11	0.30	0.71	0.08	< 0.01	1.00	0.10	< 0.01
O15347	High mobility group protein B3	0.74	0.10	< 0.01	0.67	0.10	< 0.01	1.00	0.12	< 0.01
P09429	High mobility group protein B1	0.76	0.12	< 0.01	0.71	0.13	< 0.01	1.00	0.15	< 0.01

Q03113	Guanine nucleotide-binding protein alpha-12 subunit	0.73	0.23	0.02	0.70	0.27	< 0.01	0.99	0.21	< 0.01
P14314	Glucosidase 2 subunit beta	0.81	0.10	< 0.01	0.61	0.09	< 0.01	0.99	0.09	< 0.01
O14979	Heterogeneous nuclear ribonucleoprotein D-like	0.87	0.10	< 0.01	0.71	0.10	< 0.01	0.98	0.08	< 0.01
P41250	Glycyl-tRNA synthetase	0.70	0.06	< 0.01	0.69	0.08	< 0.01	0.98	0.08	< 0.01
Q99729	Heterogeneous nuclear ribonucleoprotein A/B	0.71	0.09	< 0.01	0.66	0.10	< 0.01	0.97	0.08	< 0.01
Q15427	Splicing factor 3B subunit 4	0.86	0.14	0.06	0.71	0.12	< 0.01	0.95	0.07	< 0.01
Q14103	Heterogeneous nuclear ribonucleoprotein D0	0.83	0.07	< 0.01	0.71	0.07	< 0.01	0.95	0.06	< 0.01
Q05682	Caldesmon	0.64	0.15	< 0.01	0.81	0.18	< 0.01	0.94	0.21	< 0.01
Q96C86	Scavenger mRNA-decapping enzyme DcpS	0.81	0.08	0.09	0.70	0.09	< 0.01	0.94	0.09	< 0.01
P52566	Rho GDP-dissociation inhibitor 2	0.74	0.16	0.36	0.59	0.14	< 0.01	0.93	0.12	0.02
P49023	Paxillin	0.65	0.08	< 0.01	0.71	0.08	< 0.01	0.93	0.11	0.04
O95678	Keratin, type II cytoskeletal 75	0.79	0.06	< 0.01	0.68	0.06	< 0.01	0.91	0.05	< 0.01
Q03252	Lamin-B2	0.71	0.06	< 0.01	0.67	0.08	< 0.01	0.91	0.07	< 0.01
Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	0.82	0.19	< 0.01	0.71	0.21	< 0.01	0.90	0.20	< 0.01
P02538	Keratin, type II cytoskeletal 6A	0.75	0.08	< 0.01	0.68	0.08	< 0.01	0.90	0.07	< 0.01
Q9UQ35	Serine/arginine repetitive matrix protein 2	0.74	0.09	< 0.01	0.69	0.10	< 0.01	0.90	0.09	< 0.01
P55795	Heterogeneous nuclear ribonucleoprotein H2	0.76	0.05	< 0.01	0.69	0.06	< 0.01	0.90	0.06	< 0.01
P51114	Fragile X mental retardation syndrome-related protein 1	0.70	0.13	< 0.01	0.74	0.16	0.05	0.89	0.15	0.03
P23246	Splicing factor, proline- and glutamine-rich	0.68	0.05	< 0.01	0.64	0.05	< 0.01	0.89	0.05	< 0.01
Q9Y2Q3	Glutathione S-transferase kappa 1	0.84	0.15	< 0.01	0.71	0.12	< 0.01	0.89	0.09	< 0.01
P54727	UV excision repair protein RAD23 homolog B	0.73	0.07	< 0.01	0.65	0.07	< 0.01	0.88	0.05	< 0.01
Q13813	Spectrin alpha chain, brain	0.65	0.05	< 0.01	0.76	0.07	< 0.01	0.88	0.06	< 0.01
P61978	Heterogeneous nuclear ribonucleoprotein K	0.76	0.05	< 0.01	0.67	0.05	< 0.01	0.88	0.05	< 0.01
O43592	Exportin-T	0.73	0.07	< 0.01	0.69	0.08	< 0.01	0.88	0.06	< 0.01
Q99873	Protein arginine N-methyltransferase 1	0.76	0.16	0.17	0.67	0.13	< 0.01	0.88	0.16	< 0.01
P51991	Heterogeneous nuclear ribonucleoprotein A3	0.76	0.08	< 0.01	0.64	0.08	< 0.01	0.88	0.08	0.01
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	0.66	0.05	< 0.01	0.62	0.04	< 0.01	0.88	0.06	< 0.01
P61081	NEDD8-conjugating enzyme Ubc12	0.77	0.09	< 0.01	0.70	0.09	< 0.01	0.87	0.07	< 0.01
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	0.75	0.06	< 0.01	0.71	0.07	< 0.01	0.87	0.05	< 0.01
P05198	Eukaryotic translation initiation factor 2 subunit 1	0.72	0.10	0.06	0.69	0.10	< 0.01	0.87	0.10	< 0.01
Q9NTK5	Obg-like ATPase 1	0.75	0.08	< 0.01	0.69	0.09	< 0.01	0.87	0.08	< 0.01
Q8TBX8	Phosphatidylinositol-5-phosphate 4-kinase type-2 gamma	0.82	0.35	< 0.01	0.69	0.22	< 0.01	0.87	0.22	< 0.01
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	0.75	0.06	< 0.01	0.69	0.06	< 0.01	0.87	0.05	< 0.01
O43290	U4/U6.U5 tri-snRNP-associated protein 1	0.64	0.10	< 0.01	0.63	0.13	< 0.01	0.86	0.12	< 0.01
Q86UP2	Kinectin	0.55	0.06	< 0.01	0.67	0.07	< 0.01	0.86	0.09	0.01

Q15075	Early endosome antigen 1	0.77	0.11	< 0.01	0.69	0.10	< 0.01	0.86	0.13	< 0.01
P55263	Adenosine kinase	0.77	0.11	< 0.01	0.68	0.12	< 0.01	0.86	0.11	< 0.01
P62888	60S ribosomal protein L30 Glyoxylate	0.69	0.07	< 0.01	0.64	0.08	< 0.01	0.86	0.08	0.01
Q9UBQ7	reductase/hydroxypyruvate reductase	0.74	0.17	< 0.01	0.69	0.17	< 0.01	0.85	0.19	0.04
O76021	Ribosomal L1 domain-containing protein 1	0.75	0.08	< 0.01	0.71	0.09	< 0.01	0.85	0.09	< 0.01
P26196	Probable ATP-dependent RNA helicase DDX6	0.73	0.05	< 0.01	0.69	0.07	< 0.01	0.85	0.06	< 0.01
P20042	Eukaryotic translation initiation factor 2 subunit 2	0.79	0.10	0.97	0.70	0.08	< 0.01	0.85	0.09	0.03
Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	0.59	0.09	< 0.01	0.58	0.08	< 0.01	0.85	0.10	< 0.01
P84243	Histone H3.3	0.65	0.08	< 0.01	0.66	0.08	< 0.01	0.84	0.10	< 0.01
O43684	Mitotic checkpoint protein BUB3	0.67	0.09	< 0.01	0.65	0.12	< 0.01	0.84	0.09	0.01
P05787	Keratin, type II cytoskeletal 8	0.69	0.04	< 0.01	0.77	0.05	< 0.01	0.84	0.05	< 0.01
P41252	Isoleucyl-tRNA synthetase, cytoplasmic	0.70	0.06	< 0.01	0.72	0.07	< 0.01	0.84	0.07	< 0.01
Q14151	Scaffold attachment factor B2	0.78	0.10	0.02	0.67	0.09	< 0.01	0.84	0.10	< 0.01
Q14247	Src substrate cortactin	0.67	0.08	< 0.01	0.66	0.08	< 0.01	0.84	0.09	< 0.01
Q9Y696	Chloride intracellular channel protein 4	0.69	0.12	< 0.01	0.69	0.13	< 0.01	0.84	0.12	< 0.01
O43776	Asparaginyl-tRNA synthetase, cytoplasmic	0.64	0.08	< 0.01	0.69	0.11	0.02	0.83	0.09	< 0.01
P18754	Regulator of chromosome condensation	0.65	0.16	< 0.01	0.72	0.17	0.05	0.83	0.19	0.05
Q08J23	tRNA (cytosine-5-)- methyltransferase NSUN2	0.73	0.07	< 0.01	0.66	0.07	< 0.01	0.83	0.07	< 0.01
P40429	60S ribosomal protein L13a	0.67	0.10	< 0.01	0.65	0.09	< 0.01	0.83	0.11	< 0.01
P06899	Histone H2B type 1-J	0.70	0.04	< 0.01	0.63	0.03	< 0.01	0.83	0.04	< 0.01
Q9Y4L1	Hypoxia up-regulated protein 1	0.63	0.09	< 0.01	0.60	0.08	< 0.01	0.83	0.10	< 0.01
P58876	Histone H2B type 1-D	0.70	0.04	< 0.01	0.62	0.03	< 0.01	0.83	0.04	< 0.01
P61086	Ubiquitin-conjugating enzyme E2 K	0.80	0.15	< 0.01	0.70	0.15	< 0.01	0.82	0.13	< 0.01
Q9BQG0	Myb-binding protein 1A	0.71	0.11	< 0.01	0.70	0.10	< 0.01	0.82	0.11	< 0.01
P35637	RNA-binding protein FUS	0.80	0.11	1.00	0.62	0.08	< 0.01	0.82	0.09	< 0.01
Q15056	Eukaryotic translation initiation factor 4H	0.80	0.16	0.99	0.62	0.13	< 0.01	0.82	0.14	0.03
O43615	Mitochondrial import inner membrane translocase subunit TIM44	0.73	0.06	< 0.01	0.69	0.07	< 0.01	0.82	0.05	< 0.01
P62937	Peptidyl-prolyl cis-trans isomerase A	0.87	0.09	< 0.01	0.67	0.08	< 0.01	0.82	0.08	< 0.01
P35268	60S ribosomal protein L22	0.69	0.06	< 0.01	0.62	0.07	< 0.01	0.82	0.06	< 0.01
P78527	DNA-dependent protein kinase catalytic subunit	0.69	0.04	< 0.01	0.67	0.04	< 0.01	0.82	0.04	< 0.01
O75223	Gamma-glutamylcyclotransferase	0.79	0.16	0.03	0.67	0.13	< 0.01	0.82	0.14	0.01
P52272	Heterogeneous nuclear ribonucleoprotein M	0.73	0.05	< 0.01	0.64	0.05	< 0.01	0.82	0.05	< 0.01
P23919	Thymidylate kinase	0.83	0.11	0.12	0.63	0.10	< 0.01	0.82	0.09	< 0.01
Q13442	28 kDa heat- and acid-stable phosphoprotein	0.72	0.09	< 0.01	0.58	0.08	< 0.01	0.81	0.08	< 0.01
P55884	Eukaryotic translation initiation factor 3 subunit B	0.71	0.08	< 0.01	0.69	0.09	< 0.01	0.81	0.08	< 0.01
Q9H3H3	Uncharacterized protein C11orf68	0.64	0.12	< 0.01	0.58	0.13	< 0.01	0.81	0.11	< 0.01
P08865	40S ribosomal protein SA	0.78	0.07	0.27	0.70	0.06	< 0.01	0.81	0.05	< 0.01
P62854	40S ribosomal protein S26	0.66	0.13	< 0.01	0.63	0.13	< 0.01	0.81	0.17	< 0.01

P39019	40S ribosomal protein S19	0.78	0.11	0.46	0.68	0.10	< 0.01	0.81	0.12	0.01
P62851	40S ribosomal protein S25	0.78	0.10	< 0.01	0.68	0.10	< 0.01	0.81	0.06	< 0.01
P61353	60S ribosomal protein L27	0.78	0.09	0.13	0.66	0.09	< 0.01	0.81	0.08	< 0.01
P20700	Lamin-B1	0.68	0.05	< 0.01	0.58	0.06	< 0.01	0.81	0.05	< 0.01
P08243	Asparagine synthetase [glutamine-hydrolyzing]	0.40	0.10	< 0.01	0.39	0.12	< 0.01	0.81	0.14	0.03
P62081	40S ribosomal protein S7	0.74	0.05	< 0.01	0.69	0.05	< 0.01	0.80	0.03	< 0.01
P09211	Glutathione S-transferase P	0.74	0.09	< 0.01	0.69	0.08	< 0.01	0.80	0.09	< 0.01
Q13601	KRR1 small subunit processome component homolog	0.54	0.07	< 0.01	0.51	0.10	< 0.01	0.80	0.13	< 0.01
Q14137	Ribosome biogenesis protein BOP1	0.64	0.10	< 0.01	0.65	0.10	< 0.01	0.80	0.09	< 0.01
O00170	AH receptor-interacting protein	0.75	0.07	< 0.01	0.68	0.08	< 0.01	0.80	0.08	< 0.01
Q7L014	Probable ATP-dependent RNA helicase DDX46	0.71	0.11	< 0.01	0.64	0.12	< 0.01	0.80	0.11	0.03
P56192	Methionyl-tRNA synthetase, cytoplasmic	0.72	0.09	< 0.01	0.70	0.10	< 0.01	0.80	0.09	< 0.01
P14866	Heterogeneous nuclear ribonucleoprotein L	0.49	0.04	< 0.01	0.50	0.04	< 0.01	0.79	0.05	< 0.01
P0C055	Histone H2A.Z	0.70	0.04	< 0.01	0.58	0.05	< 0.01	0.79	0.04	< 0.01
O75821	Eukaryotic translation initiation factor 3 subunit G	0.72	0.09	< 0.01	0.71	0.10	< 0.01	0.79	0.09	< 0.01
Q9Y6M1	Insulin-like growth factor 2 mRNA- binding protein 2	0.65	0.08	< 0.01	0.70	0.08	< 0.01	0.79	0.09	< 0.01
Q96QK1	Vacuolar protein sorting- associated protein 35	0.74	0.09	< 0.01	0.69	0.09	< 0.01	0.79	0.09	< 0.01
P52597	Heterogeneous nuclear ribonucleoprotein F	0.72	0.04	< 0.01	0.64	0.05	< 0.01	0.79	0.04	< 0.01
Q9BZZ5	Apoptosis inhibitor 5	0.60	0.06	< 0.01	0.60	0.08	< 0.01	0.79	0.06	< 0.01
P23396	40S ribosomal protein S3	0.71	0.04	< 0.01	0.64	0.04	< 0.01	0.79	0.03	< 0.01
P62249	40S ribosomal protein S16	0.71	0.09	< 0.01	0.65	0.09	< 0.01	0.79	0.11	< 0.01
P62910	60S ribosomal protein L32	0.66	0.12	< 0.01	0.60	0.12	< 0.01	0.79	0.13	< 0.01
O75436	Vacuolar protein sorting- associated protein 26A	0.64	0.09	< 0.01	0.62	0.10	< 0.01	0.79	0.09	< 0.01
O60271	C-jun-amino-terminal kinase- interacting protein 4	0.61	0.08	< 0.01	0.64	0.10	< 0.01	0.79	0.09	< 0.01
P50402	Emerin	0.76	0.09	< 0.01	0.59	0.07	< 0.01	0.79	0.07	< 0.01
P09874	Poly [ADP-ribose] polymerase 1	0.71	0.05	< 0.01	0.68	0.05	< 0.01	0.79	0.05	< 0.01
Q00688	FK506-binding protein 3	0.71	0.13	< 0.01	0.66	0.09	< 0.01	0.79	0.11	< 0.01
P52292	Importin subunit alpha-2	1.79	0.11	< 0.01	1.45	0.10	< 0.01	0.79	0.05	< 0.01
Q9NZ45	CDGSH iron sulfur domain- containing protein 1	0.63	0.12	< 0.01	0.56	0.12	< 0.01	0.78	0.15	< 0.01
Q9P2J5	Leucyl-tRNA synthetase, cytoplasmic	0.68	0.08	< 0.01	0.71	0.10	< 0.01	0.78	0.08	< 0.01
Q9Y490	Talin-1	0.69	0.05	< 0.01	0.76	0.07	< 0.01	0.78	0.05	< 0.01
P62805	Histone H4	0.71	0.02	< 0.01	0.60	0.03	< 0.01	0.78	0.02	< 0.01
Q14157	Ubiquitin-associated protein 2- like	0.61	0.06	< 0.01	0.62	0.07	< 0.01	0.78	0.08	< 0.01
P19525	Interferon-induced, double- stranded RNA-activated protein kinase	0.83	0.18	0.05	0.71	0.21	< 0.01	0.78	0.16	< 0.01
Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31	0.62	0.12	< 0.01	0.57	0.10	< 0.01	0.78	0.13	0.04
Q9NUU7	ATP-dependent RNA helicase DDX19A	0.72	0.16	< 0.01	0.66	0.21	< 0.01	0.78	0.20	< 0.01
P19388	DNA-directed RNA polymerases I, II, and III subunit RPABC1	0.70	0.11	< 0.01	0.67	0.16	< 0.01	0.78	0.13	< 0.01
Q99615	Dnaj homolog subfamily C member 7	0.69	0.14	0.01	0.62	0.11	< 0.01	0.78	0.08	< 0.01
Q12874	Splicing factor 3A subunit 3	0.76	0.12	< 0.01	0.67	0.12	< 0.01	0.78	0.10	< 0.01

P60842	Eukaryotic initiation factor 4A-I	0.63	0.04	< 0.01	0.60	0.04	< 0.01	0.78	0.04	< 0.01
Q06210	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	0.68	0.26	0.02	0.69	0.25	0.02	0.78	0.24	0.05
P07814	Bifunctional aminoacyl-tRNA synthetase	0.69	0.06	< 0.01	0.74	0.08	< 0.01	0.77	0.06	< 0.01
Q15459	Splicing factor 3 subunit 1	0.72	0.08	< 0.01	0.67	0.09	< 0.01	0.77	0.08	< 0.01
P49006	MARCKS-related protein	0.66	0.07	< 0.01	0.60	0.07	< 0.01	0.77	0.08	< 0.01
Q99961	Endophilin-A2	0.73	0.16	0.02	0.61	0.15	< 0.01	0.77	0.18	< 0.01
Q9NVP1	ATP-dependent RNA helicase DDX18	0.65	0.07	< 0.01	0.68	0.08	< 0.01	0.77	0.07	< 0.01
P0COS8	Histone H2A type 1	0.71	0.07	< 0.01	0.57	0.07	< 0.01	0.77	0.06	< 0.01
P51809	Vesicle-associated membrane protein 7	0.77	0.16	< 0.01	0.67	0.15	< 0.01	0.77	0.12	< 0.01
P62241	40S ribosomal protein S8	0.69	0.04	< 0.01	0.62	0.04	< 0.01	0.77	0.03	< 0.01
Q9P258	Protein RCC2	0.65	0.08	< 0.01	0.59	0.07	< 0.01	0.77	0.07	< 0.01
Q3MHD2	Protein LSM12 homolog	0.69	0.14	< 0.01	0.63	0.15	< 0.01	0.77	0.13	< 0.01
P46782	40S ribosomal protein S5	0.72	0.09	< 0.01	0.63	0.08	< 0.01	0.77	0.07	< 0.01
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2	0.66	0.12	< 0.01	0.62	0.11	< 0.01	0.77	0.12	< 0.01
P13995	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	0.61	0.06	< 0.01	0.50	0.05	< 0.01	0.77	0.06	< 0.01
Q9UL46	Proteasome activator complex subunit 2	0.75	0.08	< 0.01	0.65	0.09	< 0.01	0.77	0.06	< 0.01
Q6P2E9	Enhancer of mRNA-decapping protein 4	0.66	0.17	< 0.01	0.80	0.21	< 0.01	0.77	0.24	< 0.01
P46778	60S ribosomal protein L21	0.63	0.10	< 0.01	0.65	0.09	< 0.01	0.77	0.09	< 0.01
Q9H223	EH domain-containing protein 4	0.80	0.15	0.08	0.68	0.12	< 0.01	0.76	0.12	< 0.01
Q96KP4	Cytosolic non-specific dipeptidase	0.72	0.11	< 0.01	0.66	0.12	< 0.01	0.76	0.10	< 0.01
P63173	60S ribosomal protein L38	0.66	0.11	< 0.01	0.61	0.11	< 0.01	0.76	0.13	< 0.01
Q71DI3	Histone H3.2	0.70	0.03	< 0.01	0.64	0.04	< 0.01	0.76	0.04	< 0.01
P08195	4F2 cell-surface antigen heavy chain	0.59	0.05	< 0.01	0.56	0.06	< 0.01	0.76	0.06	< 0.01
Q9UKM9	RNA-binding protein Raly	0.56	0.12	< 0.01	0.52	0.14	< 0.01	0.76	0.12	< 0.01
P62857	40S ribosomal protein S28	0.71	0.08	< 0.01	0.65	0.08	< 0.01	0.76	0.08	< 0.01
Q8NF91	Nesprin-1	0.59	0.22	< 0.01	0.67	0.26	< 0.01	0.76	0.22	< 0.01
P50914	60S ribosomal protein L14	0.69	0.05	< 0.01	0.61	0.05	< 0.01	0.76	0.05	< 0.01
Q5BKZ1	Zinc finger protein 326	0.78	0.18	0.98	0.64	0.14	< 0.01	0.76	0.17	0.02
Q07020	60S ribosomal protein L18	0.65	0.06	< 0.01	0.60	0.06	< 0.01	0.76	0.05	< 0.01
Q9BVP2	Guanine nucleotide-binding protein-like 3	0.48	0.12	< 0.01	0.50	0.14	< 0.01	0.76	0.14	0.03
O00571	ATP-dependent RNA helicase DDX3X	0.66	0.05	< 0.01	0.63	0.06	< 0.01	0.76	0.06	< 0.01
P51003	Poly(A) polymerase alpha	0.64	0.14	< 0.01	0.61	0.14	< 0.01	0.75	0.17	< 0.01
Q02543	60S ribosomal protein L18a	0.58	0.09	< 0.01	0.53	0.10	< 0.01	0.75	0.10	< 0.01
P62701	40S ribosomal protein S4, X isoform	0.70	0.05	< 0.01	0.64	0.05	< 0.01	0.75	0.05	< 0.01
O15355	Protein phosphatase 1G	0.73	0.09	< 0.01	0.67	0.08	< 0.01	0.75	0.08	< 0.01
Q00796	Sorbitol dehydrogenase	0.74	0.08	0.02	0.68	0.08	< 0.01	0.75	0.07	< 0.01
P62829	60S ribosomal protein L23	0.63	0.08	< 0.01	0.58	0.07	< 0.01	0.75	0.09	< 0.01
Q01813	6-phosphofructokinase type C	0.74	0.05	< 0.01	0.70	0.06	< 0.01	0.75	0.04	< 0.01
O95816	BAG family molecular chaperone regulator 2	0.79	0.16	0.20	0.64	0.15	< 0.01	0.75	0.16	< 0.01
P30050	60S ribosomal protein L12	0.65	0.05	< 0.01	0.58	0.05	< 0.01	0.75	0.04	< 0.01
P25398	40S ribosomal protein S12	0.81	0.36	1.00	0.65	0.31	< 0.01	0.75	0.30	0.01
Q9UHD8	Septin-9	0.71	0.07	< 0.01	0.64	0.09	< 0.01	0.75	0.07	< 0.01
O43852	Calumenin	0.57	0.23	< 0.01	0.64	0.26	< 0.01	0.74	0.23	< 0.01

Q6P2Q9	Pre-mRNA-processing-splicing factor 8	0.76	0.08	< 0.01	0.67	0.08	< 0.01	0.74	0.08	< 0.01
P49207	60S ribosomal protein L34	0.62	0.12	< 0.01	0.58	0.11	< 0.01	0.74	0.13	< 0.01
Q86YP4	Transcriptional repressor p66-alpha	0.80	0.31	1.00	0.59	0.16	< 0.01	0.74	0.19	0.01
Q13428	Treacle protein	0.70	0.16	< 0.01	0.66	0.14	< 0.01	0.74	0.14	< 0.01
Q5JTH9	RRP12-like protein	0.57	0.12	< 0.01	0.55	0.12	< 0.01	0.74	0.12	< 0.01
P46777	60S ribosomal protein L5	0.64	0.05	< 0.01	0.65	0.06	< 0.01	0.74	0.06	< 0.01
O00541	Pescadillo homolog 1	0.54	0.11	< 0.01	0.60	0.13	< 0.01	0.74	0.15	< 0.01
Q9Y5A9	YTH domain family protein 2	0.62	0.33	< 0.01	0.65	0.33	< 0.01	0.74	0.29	0.01
Q00613	Heat shock factor protein 1	0.73	0.11	0.01	0.64	0.12	< 0.01	0.74	0.10	< 0.01
O75683	Surfeit locus protein 6	0.37	0.09	< 0.01	0.43	0.14	< 0.01	0.74	0.15	< 0.01
P46776	60S ribosomal protein L27a	0.67	0.11	< 0.01	0.56	0.09	< 0.01	0.74	0.11	< 0.01
P62424	60S ribosomal protein L7a	0.64	0.05	< 0.01	0.60	0.06	< 0.01	0.74	0.04	< 0.01
Q92945	Far upstream element-binding protein 2	0.64	0.04	< 0.01	0.58	0.04	< 0.01	0.74	0.04	< 0.01
P55060	Exportin-2	0.75	0.05	< 0.01	0.70	0.05	< 0.01	0.74	0.04	< 0.01
P62280	40S ribosomal protein S11	0.63	0.08	< 0.01	0.60	0.09	< 0.01	0.74	0.09	< 0.01
O43491	Band 4.1-like protein 2	0.59	0.12	< 0.01	0.56	0.11	< 0.01	0.74	0.14	< 0.01
Q15050	Ribosome biogenesis regulatory protein homolog	0.45	0.11	< 0.01	0.45	0.12	< 0.01	0.74	0.10	< 0.01
P62753	40S ribosomal protein S6	0.70	0.05	< 0.01	0.63	0.05	< 0.01	0.74	0.04	< 0.01
P17480	Nucleolar transcription factor 1	0.69	0.17	< 0.01	0.59	0.15	< 0.01	0.74	0.09	< 0.01
P46781	40S ribosomal protein S9	0.73	0.09	< 0.01	0.65	0.09	< 0.01	0.74	0.10	0.02
P49321	Nuclear autoantigenic sperm protein	0.80	0.11	1.00	0.67	0.10	< 0.01	0.74	0.10	< 0.01
Q14166	Tubulin--tyrosine ligase-like protein 12	0.65	0.11	< 0.01	0.61	0.09	< 0.01	0.74	0.10	< 0.01
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	0.70	0.08	< 0.01	0.67	0.09	< 0.01	0.74	0.09	< 0.01
P54709	Sodium/potassium-transporting ATPase subunit beta-3	0.81	0.30	< 0.01	0.66	0.28	< 0.01	0.74	0.23	< 0.01
P55265	Double-stranded RNA-specific adenosine deaminase	0.62	0.09	< 0.01	0.61	0.09	< 0.01	0.74	0.08	< 0.01
Q8WW12	PEST proteolytic signal-containing nuclear protein	0.66	0.22	< 0.01	0.67	0.22	0.01	0.73	0.19	0.03
O43175	D-3-phosphoglycerate dehydrogenase	0.48	0.03	< 0.01	0.44	0.03	< 0.01	0.73	0.04	< 0.01
P57764	Gasdermin-D	0.67	0.25	0.11	0.63	0.24	0.02	0.73	0.21	0.04
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	0.72	0.05	< 0.01	0.65	0.05	< 0.01	0.73	0.04	< 0.01
P32969	60S ribosomal protein L9	0.59	0.05	< 0.01	0.55	0.05	< 0.01	0.73	0.05	< 0.01
P26373	60S ribosomal protein L13	0.65	0.05	< 0.01	0.57	0.05	< 0.01	0.73	0.05	< 0.01
P83731	60S ribosomal protein L24	0.68	0.07	< 0.01	0.63	0.08	< 0.01	0.73	0.07	< 0.01
Q15020	Squamous cell carcinoma antigen recognized by T-cells 3	0.74	0.08	0.05	0.67	0.09	< 0.01	0.73	0.06	< 0.01
P52306	Rap1 GTPase-GDP dissociation stimulator 1	0.71	0.10	< 0.01	0.71	0.11	< 0.01	0.73	0.09	< 0.01
Q15124	Phosphoglucomutase-like protein 5	0.74	0.14	0.55	0.69	0.12	< 0.01	0.73	0.10	< 0.01
P62269	40S ribosomal protein S18	0.66	0.07	< 0.01	0.65	0.08	< 0.01	0.73	0.08	< 0.01
Q9BV20	Translation initiation factor eIF-2B subunit alpha/beta/delta-like protein	0.71	0.10	< 0.01	0.65	0.11	< 0.01	0.73	0.08	< 0.01
Q9Y266	Nuclear migration protein nudC	0.81	0.07	0.07	0.71	0.07	< 0.01	0.73	0.06	< 0.01
P62917	60S ribosomal protein L8	0.65	0.09	< 0.01	0.60	0.09	< 0.01	0.73	0.09	< 0.01

Q99733	Nucleosome assembly protein 1-like 4	0.84	0.13	0.03	0.71	0.10	< 0.01	0.73	0.11	< 0.01
Q14974	Importin subunit beta-1	0.76	0.05	< 0.01	0.68	0.05	< 0.01	0.73	0.04	< 0.01
P62750	60S ribosomal protein L23a	0.62	0.07	< 0.01	0.57	0.06	< 0.01	0.73	0.05	< 0.01
Q9NR30	Nucleolar RNA helicase 2	0.69	0.05	< 0.01	0.67	0.06	< 0.01	0.73	0.05	< 0.01
P43487	Ran-specific GTPase-activating protein	0.72	0.12	< 0.01	0.64	0.12	< 0.01	0.73	0.12	< 0.01
Q8IXH7	Negative elongation factor C/D	0.64	0.15	< 0.01	0.62	0.12	< 0.01	0.73	0.13	< 0.01
Q8IY81	Putative rRNA methyltransferase 3	0.43	0.06	< 0.01	0.47	0.07	< 0.01	0.73	0.08	< 0.01
P12004	Proliferating cell nuclear antigen	0.71	0.08	< 0.01	0.65	0.08	< 0.01	0.73	0.08	< 0.01
P61247	40S ribosomal protein S3a	0.69	0.05	< 0.01	0.64	0.05	< 0.01	0.73	0.05	< 0.01
P84098	60S ribosomal protein L19	0.65	0.07	< 0.01	0.61	0.07	< 0.01	0.73	0.06	< 0.01
P42677	40S ribosomal protein S27	0.63	0.12	< 0.01	0.62	0.15	< 0.01	0.72	0.16	< 0.01
P50570	Dynamin-2	0.65	0.11	< 0.01	0.61	0.11	< 0.01	0.72	0.11	< 0.01
Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	0.42	0.06	< 0.01	0.44	0.09	< 0.01	0.72	0.10	< 0.01
Q86V81	THO complex subunit 4	0.65	0.11	< 0.01	0.51	0.10	< 0.01	0.72	0.10	< 0.01
Q9H0A0	N-acetyltransferase 10	0.51	0.05	< 0.01	0.57	0.07	< 0.01	0.72	0.06	< 0.01
O00151	PDZ and LIM domain protein 1	0.79	0.09	< 0.01	0.68	0.09	< 0.01	0.72	0.08	< 0.01
P61221	ATP-binding cassette sub-family E member 1	0.73	0.05	< 0.01	0.64	0.05	< 0.01	0.72	0.04	< 0.01
Q9UHV9	Prefoldin subunit 2	0.77	0.08	0.02	0.69	0.09	< 0.01	0.72	0.06	< 0.01
O15143	Actin-related protein 2/3 complex subunit 1B	0.79	0.24	0.94	0.68	0.16	0.02	0.72	0.16	< 0.01
P39023	60S ribosomal protein L3	0.65	0.05	< 0.01	0.64	0.06	< 0.01	0.72	0.05	< 0.01
Q92900	Regulator of nonsense transcripts 1	0.69	0.14	0.21	0.64	0.13	< 0.01	0.72	0.11	< 0.01
O15067	Phosphoribosylformylglycinamide synthase	0.76	0.09	< 0.01	0.66	0.09	< 0.01	0.72	0.08	< 0.01
P15104	Glutamine synthetase	1.20	0.24	< 0.01	1.06	0.19	< 0.01	0.65	0.16	< 0.01
P26640	Valyl-tRNA synthetase	0.90	0.15	< 0.01	0.91	0.16	< 0.01	0.66	0.09	< 0.01
P49327	Fatty acid synthase	0.79	0.03	< 0.01	0.90	0.04	< 0.01	0.61	0.02	< 0.01
P55209	Nucleosome assembly protein 1-like 1	0.88	0.09	< 0.01	0.79	0.10	< 0.01	0.67	0.07	< 0.01
P50991	T-complex protein 1 subunit delta	0.86	0.04	< 0.01	0.77	0.05	< 0.01	0.71	0.03	< 0.01
Q8TEQ6	Gem-associated protein 5	0.78	0.12	< 0.01	0.76	0.15	< 0.01	0.71	0.10	< 0.01
P04181	Ornithine aminotransferase, mitochondrial	0.74	0.07	< 0.01	0.75	0.08	0.03	0.68	0.06	< 0.01
Q9UQ80	Proliferation-associated protein 2G4	0.83	0.05	0.79	0.74	0.05	< 0.01	0.69	0.04	< 0.01
Q16204	Coiled-coil domain-containing protein 6	0.76	0.22	0.44	0.73	0.21	0.03	0.69	0.18	< 0.01
Q13045	Protein flightless-1 homolog	0.83	0.15	0.36	0.72	0.13	< 0.01	0.65	0.08	< 0.01
Q02790	FK506-binding protein 4	0.73	0.05	< 0.01	0.72	0.06	< 0.01	0.65	0.04	< 0.01
O00231	26S proteasome non-ATPase regulatory subunit 11	0.80	0.08	0.09	0.71	0.09	< 0.01	0.70	0.05	< 0.01
Q92598	Heat shock protein 105 kDa	0.77	0.03	< 0.01	0.71	0.04	< 0.01	0.67	0.03	< 0.01
P51659	Peroxisomal multifunctional enzyme type 2	0.77	0.10	0.02	0.71	0.09	< 0.01	0.66	0.08	< 0.01
Q92621	Nuclear pore complex protein Nup205	0.84	0.13	< 0.01	0.71	0.13	< 0.01	0.70	0.10	< 0.01
Q15185	Prostaglandin E synthase 3	0.83	0.10	< 0.01	0.71	0.10	< 0.01	0.69	0.07	< 0.01
Q9BSJ8	Extended-synaptotagmin-1	0.72	0.07	< 0.01	0.70	0.08	< 0.01	0.69	0.06	< 0.01
O00410	Importin-5	0.74	0.04	< 0.01	0.70	0.04	< 0.01	0.68	0.03	< 0.01

Q6UW68	Transmembrane protein 205	0.72	0.17	< 0.01	0.70	0.20	< 0.01	0.69	0.14	< 0.01
P11413	Glucose-6-phosphate 1-dehydrogenase	0.74	0.09	< 0.01	0.70	0.09	< 0.01	0.71	0.07	< 0.01
P60891	Ribose-phosphate pyrophosphokinase 1	0.75	0.08	0.04	0.69	0.08	< 0.01	0.67	0.07	< 0.01
O60232	Sjogren syndrome/scleroderma autoantigen 1	0.82	0.10	1.00	0.68	0.08	< 0.01	0.71	0.10	< 0.01
Q9HB71	Calcyclin-binding protein DNA replication licensing factor MCM2	0.77	0.06	< 0.01	0.67	0.06	< 0.01	0.68	0.05	< 0.01
P49736	Probable ATP-dependent RNA helicase DHX36	0.76	0.08	< 0.01	0.67	0.08	< 0.01	0.62	0.06	< 0.01
Q9H2U1	Trifunctional purine biosynthetic protein adenosine-3	0.78	0.13	0.82	0.66	0.10	< 0.01	0.68	0.09	< 0.01
P22102	DNA replication licensing factor MCM5	0.72	0.06	< 0.01	0.65	0.07	< 0.01	0.69	0.06	< 0.01
P11586	C-1-tetrahydrofolate synthase, cytoplasmic	0.76	0.05	< 0.01	0.65	0.04	< 0.01	0.71	0.04	< 0.01
Q9NT62	Autophagy-related protein 3	0.76	0.17	0.20	0.65	0.16	< 0.01	0.69	0.16	< 0.01
P45974	Ubiquitin carboxyl-terminal hydrolase 5	0.72	0.08	< 0.01	0.65	0.10	< 0.01	0.70	0.07	< 0.01
Q00535	Cell division protein kinase 5	0.84	0.54	< 0.01	0.65	0.47	< 0.01	0.67	0.39	< 0.01
Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1	0.69	0.26	0.10	0.65	0.22	0.02	0.69	0.31	0.03
O75475	PC4 and SFRS1-interacting protein	0.79	0.23	0.76	0.65	0.19	0.04	0.71	0.20	0.04
Q16576	Histone-binding protein RBBP7	0.73	0.14	0.02	0.65	0.15	< 0.01	0.61	0.12	< 0.01
O14893	Survival of motor neuron protein-interacting protein 1	0.87	0.22	0.23	0.64	0.15	< 0.01	0.70	0.18	< 0.01
O60678	Protein arginine N-methyltransferase 3	0.81	0.21	1.00	0.63	0.15	< 0.01	0.62	0.15	< 0.01
O14744	Protein arginine N-methyltransferase 5	0.69	0.18	0.07	0.61	0.13	0.01	0.63	0.13	< 0.01
P33993	DNA replication licensing factor MCM7	0.76	0.09	0.31	0.60	0.08	< 0.01	0.53	0.05	< 0.01
P41214	Ligatin	0.79	0.32	0.77	0.57	0.25	0.02	0.57	0.21	< 0.01
Q15645	Thyroid receptor-interacting protein 13	0.75	0.13	0.80	0.54	0.09	< 0.01	0.65	0.09	< 0.01
Q9H974	Queuine tRNA-ribosyltransferase domain-containing protein 1	0.61	0.24	0.06	0.53	0.29	0.02	0.64	0.31	0.05
P52701	DNA mismatch repair protein Msh6	0.59	0.14	0.07	0.44	0.11	< 0.01	0.53	0.12	< 0.01
P33176	Kinesin-1 heavy chain	0.45	0.47	0.07	0.42	0.41	0.04	0.47	0.40	0.04
Q13330	Metastasis-associated protein MTA1	0.40	0.45	0.08	0.19	0.23	0.03	0.24	0.29	0.03
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	0.65	0.10	< 0.01	0.71	0.12	0.05	0.86	0.10	< 0.01
P17812	CTP synthase 1	0.83	0.07	0.50	0.77	0.09	0.05	0.70	0.06	< 0.01
O75694	Nuclear pore complex protein Nup155	0.68	0.08	< 0.01	0.73	0.10	0.08	0.68	0.07	< 0.01
P53985	Monocarboxylate transporter 1	0.59	0.13	< 0.01	0.70	0.24	0.10	0.70	0.24	< 0.01
P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial	1.12	0.46	0.06	1.11	0.49	0.11	1.45	0.58	0.02
O95456	Proteasome assembly chaperone 1	0.72	0.28	0.20	0.70	0.30	0.12	0.69	0.20	< 0.01

Q9UHD1	Cysteine and histidine-rich domain-containing protein 1	0.78	0.08	0.27	0.78	0.10	0.13	0.67	0.06	< 0.01
Q9NTZ6	RNA-binding protein 12	0.78	0.21	0.81	0.65	0.24	0.14	0.70	0.17	< 0.01
P43246	DNA mismatch repair protein Msh2	0.72	0.23	0.26	0.66	0.35	0.16	0.61	0.24	0.02
O95864	Fatty acid desaturase 2	0.57	0.16	< 0.01	0.69	0.23	0.19	0.48	0.12	< 0.01
P57088	Transmembrane protein 33	0.69	0.37	0.21	0.70	0.36	0.24	0.70	0.31	0.01
O15145	Actin-related protein 2/3 complex subunit 3	0.82	1.34	1.00	0.43	0.77	0.24	0.17	0.17	0.03
Q14978	Nucleolar phosphoprotein p130	0.78	0.18	0.04	0.75	0.22	0.28	0.68	0.18	< 0.01
Q01082	Spectrin beta chain, brain 1	0.70	0.08	< 0.01	0.76	0.08	0.28	0.89	0.09	0.03
Q92616	Translational activator GCN1	0.71	0.07	< 0.01	0.79	0.09	0.30	0.79	0.07	< 0.01
Q9Y2V2	Calcium-regulated heat stable protein 1	0.82	0.30	0.92	0.71	0.20	0.35	0.66	0.24	0.04
Q9Y508	RING finger protein 114	0.82	0.18	0.32	0.73	0.21	0.35	0.63	0.13	< 0.01
Q12765	Secernin-1	0.78	0.37	0.67	0.73	0.36	0.37	0.69	0.26	0.04
Q16401	26S proteasome non-ATPase regulatory subunit 5	0.69	0.12	0.02	0.72	0.15	0.40	0.73	0.10	< 0.01
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0.70	0.17	< 0.01	0.80	0.22	0.44	1.01	0.21	< 0.01
Q8N726	Cyclin-dependent kinase inhibitor 2A, isoform 4	0.70	0.33	0.44	0.78	0.36	0.47	1.51	0.59	< 0.01
P25789	Proteasome subunit alpha type-4	0.59	0.59	0.23	0.71	0.69	0.59	0.49	0.39	0.02
P78371	T-complex protein 1 subunit beta	0.86	0.05	< 0.01	0.79	0.05	0.72	0.70	0.04	< 0.01
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal	0.76	0.25	0.99	0.73	0.26	0.74	0.68	0.22	< 0.01
Q9H8Y8	Golgi reassembly-stacking protein 2	0.88	0.70	0.89	0.73	0.58	0.74	1.43	1.08	0.02
Q14694	Ubiquitin carboxyl-terminal hydrolase 10	0.85	0.19	0.51	0.80	0.24	0.79	0.68	0.21	0.01
P48643	T-complex protein 1 subunit epsilon	0.92	0.06	< 0.01	0.82	0.06	0.84	0.70	0.04	< 0.01
Q8N1F7	Nuclear pore complex protein Nup93	0.79	0.10	0.53	0.77	0.11	0.86	0.69	0.09	< 0.01
O15160	DNA-directed RNA polymerases I and III subunit RPAC1	0.80	0.16	1.00	0.75	0.19	0.87	0.69	0.13	< 0.01
P53396	ATP-citrate synthase	0.80	0.06	0.47	0.79	0.07	0.92	0.68	0.05	< 0.01
P84103	Splicing factor, arginine-serine-rich 3	1.02	0.58	< 0.01	0.82	0.48	0.99	0.27	0.22	< 0.01
P28070	Proteasome subunit beta type-4	0.56	0.55	0.10	0.72	0.84	0.99	0.58	0.51	0.05
P07305	Histone H1.0	0.74	0.18	0.68	0.83	0.23	0.99	1.62	0.38	< 0.01
P28074	Proteasome subunit beta type-5	0.50	0.48	< 0.01	0.76	0.86	1.00	0.59	0.48	0.03
Q8NBS9	Thioredoxin domain-containing protein 5	0.71	0.06	< 0.01	0.81	0.09	1.00	0.75	0.07	< 0.01
Q8N5K1	CDGSH iron sulfur domain-containing protein 2	0.76	0.16	0.45	0.62	0.11	< 0.01	0.77	0.13	0.05
Q96IU4	Abhydrolase domain-containing protein 14B	0.61	0.20	< 0.01	0.58	0.13	< 0.01	0.73	0.23	0.05
Q8WXF1	Paraspeckle component 1	0.83	0.08	0.16	0.61	0.09	< 0.01	0.97	0.13	0.05
Q8TD57	Dynein heavy chain 3, axonemal	0.79	0.32	0.89	0.70	0.19	0.04	0.76	0.24	0.05
Q16643	Drebrin	0.73	0.12	< 0.01	0.71	0.11	< 0.01	0.81	0.11	0.06

Q14980	Nuclear mitotic apparatus protein 1	0.62	0.09	< 0.01	0.64	0.11	< 0.01	0.77	0.10	0.06
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2	0.78	0.17	< 0.01	0.67	0.23	< 0.01	0.74	0.19	0.07
Q9BY77	Polymerase delta-interacting protein 3	0.66	0.16	< 0.01	0.60	0.17	< 0.01	0.76	0.16	0.07
Q96GQ7	Probable ATP-dependent RNA helicase DDX27	0.57	0.10	< 0.01	0.57	0.11	< 0.01	0.79	0.13	0.08
Q9BRJ6	Uncharacterized protein C7orf50	0.33	0.18	< 0.01	0.39	0.20	< 0.01	0.71	0.28	0.08
Q9NZJ4	Sacsin	0.68	0.22	0.02	0.85	0.30	0.11	0.96	0.33	0.08
Q9UHD9	Ubiquilin-2	0.75	0.12	0.07	0.67	0.17	< 0.01	0.90	0.10	0.08
Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	0.75	0.13	0.04	0.64	0.11	< 0.01	0.80	0.11	0.08
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1	0.54	0.13	< 0.01	0.52	0.14	< 0.01	0.73	0.18	0.11
Q13098	COP9 signalosome complex subunit 1	0.71	0.27	0.08	0.63	0.18	< 0.01	0.78	0.27	0.11
P61163	Alpha-actinin	2.02	3.13	< 0.01	1.84	2.70	0.01	1.59	2.22	0.11
P62266	40S ribosomal protein S23	0.48	0.27	0.10	0.53	0.22	0.03	0.62	0.24	0.12
Q13148	TAR DNA-binding protein 43	0.66	0.11	< 0.01	0.65	0.12	< 0.01	0.86	0.12	0.12
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	0.76	0.19	< 0.01	0.67	0.20	0.01	0.87	0.20	0.13
Q9P015	39S ribosomal protein L15, mitochondrial	1.70	0.47	< 0.01	1.44	0.53	< 0.01	1.81	1.41	0.13
Q96CT7	Coiled-coil domain-containing protein 124	0.54	0.30	< 0.01	0.46	0.27	< 0.01	0.74	0.26	0.14
Q14677	Clathrin interactor 1	0.50	0.15	< 0.01	0.67	0.22	0.04	0.74	0.18	0.15
P35080	Profilin-2	0.63	0.14	< 0.01	0.66	0.16	0.05	0.77	0.17	0.15
Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	0.60	0.26	< 0.01	0.59	0.23	< 0.01	0.76	0.28	0.16
P21399	Cytoplasmic aconitate hydratase	1.45	1.82	< 0.01	1.17	1.57	0.36	1.37	1.65	0.16
Q9Y5M8	Signal recognition particle receptor subunit beta	0.74	0.09	< 0.01	0.68	0.08	< 0.01	0.80	0.12	0.16
Q99614	Tetratricopeptide repeat protein 1	0.70	0.15	< 0.01	0.66	0.15	< 0.01	0.80	0.18	0.16
P22087	rRNA 2'-O-methyltransferase fibrillarin	0.81	0.15	0.58	0.71	0.12	0.01	0.89	0.14	0.17
Q9C010	cAMP-dependent protein kinase inhibitor beta	0.61	0.31	0.30	0.53	0.26	0.02	0.68	0.35	0.17
Q96EP5	DAZ-associated protein 1	0.71	0.19	< 0.01	0.68	0.17	< 0.01	0.83	0.21	0.18
Q9Y3D9	28S ribosomal protein S23, mitochondrial	0.67	0.23	< 0.01	0.66	0.26	< 0.01	0.79	0.29	0.19
O00425	Insulin-like growth factor 2 mRNA-binding protein 3	0.70	0.10	< 0.01	0.71	0.10	< 0.01	0.86	0.10	0.20
Q9Y3U8	60S ribosomal protein L36	0.69	0.13	< 0.01	0.63	0.14	< 0.01	0.80	0.17	0.21
Q93009	Ubiquitin carboxyl-terminal hydrolase 7	0.73	0.14	0.30	0.64	0.14	< 0.01	0.82	0.13	0.21
P62158	Calmodulin	0.78	0.13	1.00	0.67	0.10	< 0.01	0.85	0.11	0.22
P25325	3-mercaptopyruvate sulfurtransferase	0.81	0.19	0.97	0.64	0.17	< 0.01	0.96	0.16	0.22
P33240	Cleavage stimulation factor 64 kDa subunit	0.67	0.14	< 0.01	0.70	0.15	0.02	0.82	0.14	0.22
Q9H2D6	TRIO and F-actin-binding protein	0.61	0.22	0.03	0.86	0.56	0.82	0.72	0.42	0.22
Q13564	NEDD8-activating enzyme E1 regulatory subunit	0.76	0.18	0.65	0.70	0.16	< 0.01	0.83	0.12	0.24
Q15397	Pumilio domain-containing protein KIAA0020	0.76	0.24	0.61	0.54	0.20	< 0.01	0.93	0.20	0.25

Q9H9P8	L-2-hydroxyglutarate dehydrogenase, mitochondrial	0.75	0.19	0.17	0.69	0.17	< 0.01	0.94	0.14	0.28
Q9UKD2	mRNA turnover protein 4 homolog	0.73	0.11	< 0.01	0.64	0.12	< 0.01	0.83	0.12	0.28
Q13151	Heterogeneous nuclear ribonucleoprotein A0	0.68	0.08	< 0.01	0.59	0.06	< 0.01	0.89	0.09	0.29
P62633	Cellular nucleic acid-binding protein	0.43	0.13	< 0.01	0.53	0.15	< 0.01	0.73	0.19	0.31
P55735	Protein SEC13 homolog	0.64	0.23	< 0.01	0.57	0.21	< 0.01	0.71	0.52	0.31
P18615	Negative elongation factor E	0.70	0.20	0.04	0.67	0.14	< 0.01	0.89	0.24	0.32
Q15166	Serum paraoxonase/lactonase 3	0.67	0.19	< 0.01	0.67	0.23	0.02	0.97	0.25	0.35
O94906	Pre-mRNA-processing factor 6	0.71	0.18	0.02	0.71	0.16	0.07	0.84	0.24	0.36
Q15637	Splicing factor 1	0.71	0.09	< 0.01	0.68	0.13	< 0.01	0.84	0.11	0.37
P31943	Heterogeneous nuclear ribonucleoprotein H	0.76	0.05	< 0.01	0.68	0.05	< 0.01	0.87	0.05	0.37
P23193	Transcription elongation factor A protein 1	0.67	0.18	< 0.01	0.59	0.17	< 0.01	1.01	0.24	0.38
P41567	Eukaryotic translation initiation factor 1	0.65	0.12	< 0.01	0.54	0.09	< 0.01	0.99	0.17	0.38
Q9Y3Z3	SAM domain and HD domain-containing protein 1	0.71	0.13	0.06	0.61	0.15	< 0.01	0.80	0.11	0.39
P28066	Proteasome subunit alpha type-5	0.63	0.22	0.03	0.85	0.30	0.57	0.93	0.27	0.44
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	0.88	0.30	0.45	0.70	0.21	< 0.01	1.00	0.31	0.44
Q96KR1	Zinc finger RNA-binding protein	0.61	0.17	< 0.01	0.69	0.23	0.03	0.73	0.18	0.45
Q5SSJ5	Heterochromatin protein 1-binding protein 3	0.71	0.26	< 0.01	0.65	0.16	< 0.01	0.86	0.20	0.46
Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein	0.78	0.14	0.64	0.67	0.10	0.01	0.96	0.18	0.47
P62273	40S ribosomal protein S29	0.75	0.64	1.00	0.51	0.38	< 0.01	0.73	0.50	0.47
Q15424	Scaffold attachment factor B1	0.82	0.14	1.00	0.67	0.12	< 0.01	0.86	0.13	0.48
Q16555	Dihydropyrimidinase-related protein 2	0.61	0.18	< 0.01	0.69	0.17	0.06	0.82	0.25	0.48
P29317	Ephrin type-A receptor 2	0.60	0.29	< 0.01	0.55	0.27	< 0.01	0.81	0.30	0.49
P56182	Ribosomal RNA processing protein 1 homolog A	0.50	0.14	< 0.01	0.55	0.14	< 0.01	0.79	0.17	0.49
P20929	Nebulin	0.74	0.09	< 0.01	0.66	0.09	< 0.01	0.87	0.09	0.49
P54577	Tyrosyl-tRNA synthetase, cytoplasmic	0.62	0.05	< 0.01	0.58	0.05	< 0.01	0.84	0.06	0.50
Q92552	28S ribosomal protein S27, mitochondrial	0.85	0.17	0.95	0.70	0.15	< 0.01	0.95	0.15	0.52
P51572	B-cell receptor-associated protein 31	0.60	0.17	< 0.01	0.68	0.27	0.23	0.78	0.29	0.54
Q15233	Non-POU domain-containing octamer-binding protein	0.71	0.05	< 0.01	0.66	0.06	< 0.01	0.90	0.06	0.57
Q96QD8	Sodium-coupled neutral amino acid transporter 2	0.59	0.09	< 0.01	0.59	0.12	< 0.01	0.96	0.16	0.59
P12931	Proto-oncogene tyrosine-protein kinase Src	0.54	0.10	< 0.01	0.56	0.09	< 0.01	0.84	0.11	0.62
	NADH dehydrogenase									
O00217	[ubiquinone] iron-sulfur protein 8, mitochondrial	0.81	0.21	1.00	0.64	0.16	< 0.01	0.97	0.21	0.63
P54886	Delta-1-pyrroline-5-carboxylate synthetase	0.70	0.08	< 0.01	0.68	0.09	< 0.01	0.86	0.09	0.68
O43847	Nardilysin	0.74	0.26	0.27	0.59	0.19	< 0.01	0.85	0.18	0.69
Q9UHY7	Enolase-phosphatase E1	0.74	0.23	0.10	0.69	0.16	< 0.01	0.97	0.27	0.70

P04264	Keratin, type II cytoskeletal 1	0.56	0.13	< 0.01	0.40	0.13	< 0.01	0.80	0.20	0.71
O00193	Small acidic protein	0.69	0.14	< 0.01	0.64	0.13	< 0.01	0.95	0.19	0.76
P48739	Phosphatidylinositol transfer protein beta isoform	0.85	0.20	0.79	0.70	0.17	< 0.01	0.86	0.18	0.78
Q96CX2	BTB/POZ domain-containing protein KCTD12	0.66	0.26	0.02	0.75	0.34	0.92	0.80	0.35	0.78
Q92522	Histone H1x	0.60	0.25	< 0.01	0.44	0.21	< 0.01	0.95	0.31	0.81
Q15717	ELAV-like protein 1	0.66	0.08	< 0.01	0.64	0.10	< 0.01	0.84	0.11	0.81
Q8WVJ2	NudC domain-containing protein 2	0.73	0.21	0.61	0.66	0.19	< 0.01	0.82	0.21	0.81
A6NL28	Putative tropomyosin alpha-3 chain-like protein	0.79	0.15	0.16	0.71	0.12	< 0.01	0.90	0.14	0.82
P46783	40S ribosomal protein S10	0.60	0.35	< 0.01	0.60	0.55	0.02	0.77	0.50	0.84
Q6FI81	Anamorsin	0.69	0.66	0.86	0.54	0.57	0.02	0.77	0.53	0.85
P13645	Keratin, type I cytoskeletal 10	0.62	0.14	< 0.01	0.55	0.14	< 0.01	0.69	0.24	0.86
Q53EL6	Programmed cell death protein 4	0.42	0.15	< 0.01	0.50	0.13	< 0.01	0.95	0.21	0.86
Q9UJ72	Annexin A10	0.68	0.38	0.27	0.61	0.27	0.03	0.92	0.37	0.86
P08708	40S ribosomal protein S17	0.70	0.34	0.05	0.59	0.28	0.03	0.72	0.38	0.87
P82675	28S ribosomal protein S5, mitochondrial	0.79	0.09	< 0.01	0.69	0.12	< 0.01	0.88	0.12	0.87
Q96I24	Far upstream element-binding protein 3	0.64	0.12	< 0.01	0.60	0.12	< 0.01	0.87	0.15	0.87
O43768	Alpha-endosulfine	0.66	0.24	< 0.01	0.58	0.16	< 0.01	0.81	0.19	0.87
P36507	Dual specificity mitogen-activated protein kinase kinase 2	0.64	0.20	< 0.01	0.74	0.19	0.11	0.86	0.36	0.87
Q9HCD5	Nuclear receptor coactivator 5	0.49	0.23	< 0.01	0.59	0.26	< 0.01	0.96	0.57	0.88
P26583	High mobility group protein B2	0.64	0.11	< 0.01	0.59	0.11	< 0.01	0.82	0.15	0.92
Q8WXX5	DnaJ homolog subfamily C member 9	0.83	0.11	< 0.01	0.69	0.08	< 0.01	0.90	0.11	0.92
P35222	Catenin beta-1	0.65	0.25	< 0.01	0.70	0.28	0.03	0.95	0.36	0.94
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	0.67	0.09	< 0.01	0.60	0.09	< 0.01	0.92	0.12	0.95
Q15269	Periodic tryptophan protein 2 homolog	0.75	0.12	0.38	0.70	0.13	< 0.01	0.89	0.15	0.95
Q13263	Transcription intermediary factor 1-beta	0.72	0.06	< 0.01	0.65	0.06	< 0.01	0.85	0.07	0.95
Q96DH6	RNA-binding protein Musashi homolog 2	0.65	0.10	< 0.01	0.64	0.11	< 0.01	0.88	0.13	0.96
P49588	Alanyl-tRNA synthetase, cytoplasmic	0.56	0.04	< 0.01	0.59	0.05	< 0.01	0.90	0.05	0.96
Q9BWF3	RNA-binding protein 4	0.70	0.17	0.02	0.66	0.19	< 0.01	0.94	0.26	0.98
O94925	Glutaminase kidney isoform, mitochondrial	0.70	0.15	< 0.01	0.72	0.14	0.06	0.88	0.19	0.98
P35527	Keratin, type I cytoskeletal 9	0.48	0.46	0.20	0.31	0.36	< 0.01	0.93	1.23	0.99
Q9NZT2	Opioid growth factor receptor	0.64	0.11	< 0.01	0.64	0.14	< 0.01	0.83	0.15	0.99
O60749	Sorting nexin-2	0.78	0.39	1.00	0.60	0.28	0.01	0.85	0.33	0.99
Q9NVA2	Septin-11	0.66	0.16	< 0.01	0.69	0.19	< 0.01	0.86	0.21	1.00
Q96SZ5	2-aminoethanethiol dioxygenase	0.61	0.29	< 0.01	0.70	0.34	0.10	0.96	0.57	1.00
P05386	60S acidic ribosomal protein P1	0.82	0.23	1.00	0.59	0.24	< 0.01	0.75	0.52	1.00
Q13595	Transformer-2 protein homolog	0.74	0.12	< 0.01	0.67	0.16	< 0.01	0.92	0.15	1.00
Q6DKI1	60S ribosomal protein L7-like 1	0.60	0.18	< 0.01	0.56	0.23	< 0.01	0.94	0.34	1.00
Q9GZP4	UPF0424 protein C1orf128	0.66	0.23	< 0.01	0.81	0.37	1.00	0.88	0.33	1.00

O60739	Eukaryotic translation initiation factor 1b	0.64	0.13	< 0.01	0.55	0.10	< 0.01	0.96	0.20	1.00
Q7RTV0	PHD finger-like domain-containing protein 5A	0.66	0.16	< 0.01	0.69	0.24	0.04	0.89	0.26	1.00
Q86U42	Polyadenylate-binding protein 2	0.72	0.15	0.01	0.61	0.11	< 0.01	0.89	0.13	1.00
P35908	Keratin, type II cytoskeletal 2 epidermal	0.73	0.10	< 0.01	0.63	0.10	< 0.01	0.93	0.09	1.00
P18827	Syndecan-1	0.65	0.13	< 0.01	0.47	0.10	< 0.01	0.89	0.19	1.00
O75368	SH3 domain-binding glutamic acid-rich-like protein	0.65	0.23	< 0.01	0.68	0.28	< 0.01	0.89	0.31	1.00
P84090	Enhancer of rudimentary homolog	0.74	0.14	0.31	0.65	0.12	< 0.01	0.92	0.14	1.00